ATCC 31,195 ALPHA-AMYLASE AMINO ACID SEQUENCE

```
  1 aapfngtmmq yfewylpddg tlwtkvanea nnlsslgita lwlppaykgt srsdvgygvy
 61 dlydlgefnq kgtvrtkygt kaqylqaiqa ahaagmqvya dvvfdhkgga dgtewvdave
121 vnpsdrnqei sgtyqiqawt kfdfpgrgnt yssfkwrwyh fdgvdwdesr klsriykfrg
181 igkawdwevd tengnydylm yadldmdhpe vvtelknwgk wyvnttnidg frldavkhik
241 fsffpdwlsy vrsqtgkplf tvgeywsydi nklhnyitkt ngtmslfdap lhnkfytask
301 sggafdmrtl mtntlmkdqp tlavtfvdnh dtepgqalqs wvdpwfkpla yafiltrqeg
361 ypcvfygdyy gipqynipsl kskidpllia rrdyaygtqh dyldhsdiig wtregvtekp
421 gsglaalitd gpggskwmyv gkqhagkvfy dltgnrsdtv tinsdgwgef kvnggsvsvw
481 vprkttvst
```

EXHIBIT 5

GAP ALIGNMENT:
ATCC 31,195 Alpha-Amylase to Spezyme Ethyl (Old Matrix)

```
 GAP of: NewC.pep  check: 5818  from: 1  to: 489

WPDEF ATCC 31,195 ALPHA-AMYLASE AMINO ACID SEQUENCE
None

 to: SPEZE.pep  check: 525  from: 1  to: 484

WPDEF SPEZYME® ETHYL AMINO ACID SEQUENCE
None

 Symbol comparison table: oldpep.cmp CompCheck: 2543
Dayhoff table (Schwartz, R. M. and Dayhoff, M. O. [1979] in Atlas of
Protein Sequence and Structure, Dayhoff, M. O. Ed, pp. 353-358, National
Biomedical Research Foundation, Washington D.C.) rescaled by dividing
each value by the sum of its row and column, and normalizing to a mean
of 0 and standard deviation of 1.0.  The value for FY (Phe-Tyr) = RW =
1.425.  Perfect matches are set to 1.5 and no matches on any row are . . .

        Gap Weight:     30      Average Match:  5.402
     Length Weight:      3   Average Mismatch: -3.964

           Quality:   7224             Length:    489
             Ratio: 14.926               Gaps:      1
Percent Similarity: 100.000   Percent Identity: 100.000

       Match display thresholds for the alignment(s):
                   | = IDENTITY
                   : =   4
                   . =   1

NewC.pep x SPEZE.pep      June 11, 2005 12:05  ..

                .         .         .         .         .
      1 aapfngtmmqyfewylpddgtlwtkvaneannlsslgitalwlppaykgt 50
        |||||||||||||||||||||||||||||||||||||||||||||||||||
      1 AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNLSSLGITALWLPPAYKGT 50
                .         .         .         .         .
     51 srsdvgygvydlydlgefnqkgtvrtkygtkaqylqaiqaahaagmqvya 100
        |||||||||||||||||||||||||||||||||||||||||||||||||||
     51 SRSDVGYGVYDLYDLGEFNQKGTVRTKYGTKAQYLQAIQAAHAAGMQVYA 100
                .         .         .         .         .
    101 dvvfdhkggadgtewvdavevnpsdrnqeisgtyqiqawtkfdfpgrgnt 150
        |||||||||||||||||||||||||||||||||||||||||||||||||||
    101 DVVFDHKGGADGTEWVDAVEVNPSDRNQEISGTYQIQAWTKFDFPGRGNT 150
                .         .         .         .         .
    151 yssfkwrwyhfdgvdwdesrklsriykfrgigkawdwevdtengnydylm 200
        |||||||||||||||||||||||||||  ||||||||||||||||||||
    151 YSSFKWRWYHFDGVDWDESRKLSRIYKF..IGKAWDWEVDTENGNYDYLM 198
                .         .         .         .         .
    201 yadldmdhpevvtelknwgkwyvnttnidgfrldavkhikfsffpdwlsy 250
        |||||||||||||||||||||||||||||||||||||||||||||||||||
    199 YADLDMDHPEVVTELKNWGKWYVNTTNIDGFRLDAVKHIKFSFFPDWLSY 248
```

GAP Alignment:
ATCC 31,195 Alpha-Amylase to Spezyme Ethyl
(Old Matrix)

```
                .         .         .         .         .
251 vrsqtgkplftvgeywsydinklhnyitktngtmslfdaplhnkfytask 300
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
249 VRSQTGKPLFTVGEYWSYDINKLHNYITKTNGTMSLFDAPLHNKFYTASK 298
                .         .         .         .         .
301 sggafdmrtlmtntlmkdqptlavtfvdnhdtepgqalqswvdpwfkpla 350
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
299 SGGAFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWVDPWFKPLA 348
                .         .         .         .         .
351 yafiltrqegypcvfygdyygipqynipslkskidplliarrdyaygtqh 400
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
349 YAFILTRQEGYPCVFYGDYYGIPQYNIPSLKSKIDPLLIARRDYAYGTQH 398
                .         .         .         .         .
401 dyldhsdiigwtregvtekpgsglaalitdgpggskwmyvgkqhagkvfy 450
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
399 DYLDHSDIIGWTREGVTEKPGSGLAALITDGPGGSKWMYVGKQHAGKVFY 448
                .         .         .
451 dltgnrsdtvtinsdgwgefkvnggsvsvwvprkttvst 489
    |||||||||||||||||||||||||||||||||||||
449 DLTGNRSDTVTINSDGWGEFKVNGGSVSVWVPRKTT... 484
```

EXHIBIT 6

GAP ALIGNMENT:
ATCC 31,195 Alpha-Amylase to Spezyme Ethyl (New Matrix)

```
 GAP of: NewC.pep  check: 5818  from: 1  to: 489

WPDEF ATCC 31,195 ALPHA-AMYLASE AMINO ACID SEQUENCE
None

 to: SPEZE.pep  check: 525  from: 1  to: 484

WPDEF SPEZYME® ETHYL AMINO ACID SEQUENCE
None

 Symbol comparison table: blosum62.cmp CompCheck: 1102
BLOSUM62 amino acid substitution matrix.
Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid
           substitution matrices from protein blocks.  Proc. Natl. Acad.
           Sci. USA 89: 10915-10919.

         Gap Weight:      8      Average Match:  2.778
      Length Weight:      2   Average Mismatch: -2.248

            Quality:   2665              Length:    489
              Ratio:  5.506               Gaps:      1
 Percent Similarity: 100.000   Percent Identity: 100.000

        Match display thresholds for the alignment(s):
                    | = IDENTITY
                    : =   2
                    . =   1

 NewC.pep x SPEZE.pep      June 11, 2005 12:01  ..

                .         .         .         .         .
       1 aapfngtmmqyfewylpddgtlwtkvaneannlsslgitalwlppaykgt 50
         |||||||||||||||||||||||||||||||||||||||||||||||||||
       1 AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNLSSLGITALWLPPAYKGT 50
                .         .         .         .         .
      51 srsdvgygvydlydlgefnqkgtvrtkygtkaqylqaiqaahaagmqvya 100
         |||||||||||||||||||||||||||||||||||||||||||||||||||
      51 SRSDVGYGVYDLYDLGEFNQKGTVRTKYGTKAQYLQAIQAAHAAGMQVYA 100
                .         .         .         .         .
     101 dvvfdhkggadgtewvdavevnpsdrnqeisgtyqiqawtkfdfpgrgnt 150
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     101 DVVFDHKGGADGTEWVDAVEVNPSDRNQEISGTYQIQAWTKFDFPGRGNT 150
                .         .         .         .         .
     151 yssfkwrwyhfdgvdwdesrklsriykfrgigkawdwevdtengnydylm 200
         |||||||||||||||||||||||||||  ||||||||||||||||||||
     151 YSSFKWRWYHFDGVDWDESRKLSRIYKF..IGKAWDWEVDTENGNYDYLM 198
                .         .         .         .         .
     201 yadldmdhpevvtelknwgkwyvnttnidgfrldavkhikfsffpdwlsy 250
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     199 YADLDMDHPEVVTELKNWGKWYVNTTNIDGFRLDAVKHIKFSFFPDWLSY 248
                .         .         .         .         .
     251 vrsqtgkplftvgeywsydinklhnyitktngtmslfdaplhnkfytask 300
```

GAP Alignment:
ATCC 31,195 Alpha-Amylase to Spezyme Ethyl
(New Matrix)

```
                                                                    
249 VRSQTGKPLFTVGEYWSYDINKLHNYITKTNGTMSLFDAPLHNKFYTASK 298
                                                                    
301 sggafdmrtlmtntlmkdqptlavtfvdnhdtepgqalqswvdpwfkpla 350
                                                                    
299 SGGAFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWVDPWFKPLA 348
                                                                    
351 yafiltrqegypcvfygdyygipqynipslkskidplliarrdyaygtqh 400
                                                                    
349 YAFILTRQEGYPCVFYGDYYGIPQYNIPSLKSKIDPLLIARRDYAYGTQH 398
                                                                    
401 dyldhsdiigwtregvtekpgsglaalitdgpggskwmyvgkqhagkvfy 450
                                                                    
399 DYLDHSDIIGWTREGVTEKPGSGLAALITDGPGGSKWMYVGKQHAGKVFY 448
                                                                    
451 dltgnrsdtvtinsdgwgefkvnggsvsvwvprkttvst 489
                                                                    
449 DLTGNRSDTVTINSDGWGEFKVNGGSVSVWVPRKTT... 484
```

EXHIBIT 7

GAP ALIGNMENT:
SEQ ID NO:3 to Spezyme Ethyl (Old Matrix)

GAP of: NewB.pep check: 1170 from: 1 to: 514

WPDEF Seq ID Nos 3, translated by ThreeToOne
none

to: SPEZE.pep check: 525 from: 1 to: 484

WPDEF SPEZYME® ETHYL AMINO ACID SEQUENCE
None

Symbol comparison table: oldpep.cmp CompCheck: 2543
Dayhoff table (Schwartz, R. M. and Dayhoff, M. O. [1979] in Atlas of Protein Sequence and Structure, Dayhoff, M. O. Ed, pp. 353-358, National Biomedical Research Foundation, Washington D.C.) rescaled by dividing each value by the sum of its row and column, and normalizing to a mean of 0 and standard deviation of 1.0. The value for FY (Phe-Tyr) = RW = 1.425. Perfect matches are set to 1.5 and no matches on any row are . . .

Gap Weight:	30	Average Match:	5.402
Length Weight:	3	Average Mismatch:	-3.964
Quality:	7155	Length:	514
Ratio:	14.783	Gaps:	1
Percent Similarity:	99.380	Percent Identity:	98.967

Match display thresholds for the alignment(s):
| = IDENTITY
: = 4
. = 1

NewB.pep x SPEZE.pep June 3, 2005 11:08 ..

```
          .         .         .         .         .
  1 AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNLSSLGITALWLPPAYKGT 50
    |||||||||||||||||||||||||||||||||||||||||||||||||||
  1 AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNLSSLGITALWLPPAYKGT 50
          .         .         .         .         .
 51 SRSDVGYGVYDLYDLGEFNQKGAVRTKYGTKAQYLQAIQAAHAAGMQVYA 100
    ||||||||||||||||||||||:|||||||||||||||||||||||||||
 51 SRSDVGYGVYDLYDLGEFNQKGTVRTKYGTKAQYLQAIQAAHAAGMQVYA 100
          .         .         .         .         .
101 DVVFDHKGGADGTEWVDAVEVNPSDRNQEISGTYQIQAWTKFDFPGRGNT 150
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
101 DVVFDHKGGADGTEWVDAVEVNPSDRNQEISGTYQIQAWTKFDFPGRGNT 150
          .         .         .         .         .
151 YSSFKWRWYHFDGVDWDESRKLSRIYKFRGIGKAWDWEVDTENGNYDYLM 200
    |||||||||||||||||||||||||||  ||||||||||||||||||||
151 YSSFKWRWYHFDGVDWDESRKLSRIYKF..IGKAWDWEVDTENGNYDYLM 198
          .         .         .         .         .
201 YADLDMDHPEVVTELKSWGKWYVNTTNIDGFRLDAVKHIKFSFFPDWLSD 250
    |||||||||||||||.||||||||||||||||||||||||||||||||||
199 YADLDMDHPEVVTELKNWGKWYVNTTNIDGFRLDAVKHIKFSFFPDWLSY 248
```

GAP Alignment:
SEQ ID NO:3 to Spezyme Ethyl
(Old Matrix)

```
251 VRSQTGKPLFTVGEYWSYDINKLHNYIMKTNGTMSLFDAPLHNKFYTASK 300
    ||||||||||||||||||||||||||| ||||||||||||||||||||||
249 VRSQTGKPLFTVGEYWSYDINKLHNYITKTNGTMSLFDAPLHNKFYTASK 298

301 SGGTFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWVDPWFKPLA 350
    |||:||||||||||||||||||||||||||||||||||||||||||||||
299 SGGAFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWVDPWFKPLA 348

351 YAFILTRQEGYPCVFYGDYYGIPQYNIPSLKSKIDPLLIARRDYAYGTQH 400
    ||||||||||||||||||||||||||||||||||||||||||||||||||
349 YAFILTRQEGYPCVFYGDYYGIPQYNIPSLKSKIDPLLIARRDYAYGTQH 398

401 DYLDHSDIIGWTREGVTEKPGSGLAALITDGPGGSKWMYVGKQHAGKVFY 450
    ||||||||||||||||||||||||||||||||||||||||||||||||||
399 DYLDHSDIIGWTREGVTEKPGSGLAALITDGPGGSKWMYVGKQHAGKVFY 448

451 DLTGNRSDTVTINSDGWGEFKVNGGSVSVWVPRKTTVSTIAWSITTRPWT 500
    ||||||||||||||||||||||||||||||||||
449 DLTGNRSDTVTINSDGWGEFKVNGGSVSVWVPRKTT.............. 484
```

EXHIBIT 8